

**S001** Protein mass spectrometry and the identification of post-translational modifications

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Modern mass spectrometric methods provide a formidable armamentarium to enable both the qualitative and quantitative determination of oxidative modifications of proteins and other types of post-translational modification (PTM). The combination of soft ionisation methods and tandem mass spectrometry facilitates the analysis of intact proteins and of proteolytic peptides whose characterisation provides detail concerning the site and nature of the structural modification. A key analytical challenge is the determination of structural modifications occurring with very low stoichiometry, as is commonly the case with regard to oxidative modification and PTMs such as phosphorylation. This challenge may be addressed in a number of ways, including the use of tandem mass spectrometry to achieve selective detection based on ion fragmentation properties unique to the structure of interest. With regard to the determination of the stoichiometry of protein modification (and the absolute quantification of specific proteins), new approaches are emerging based on the principles of stable isotope dilution.